



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/618,839
Source: O/P
Date Processed by STIC: 7/25/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/618,839

DATE: 07/25/2003

TIME: 07:58:42

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07252003\J618839.raw

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3 <110> APPLICANT: Lambeth, J. David
4      Cheng, Guangjie
5      McCoy, James
7 <120> TITLE OF INVENTION: Methods and Transgenic Mouse Model for Identifying and
Modulating Factors
8      Involved in the Production of Reactive Oxygen Intermediates
10 <130> FILE REFERENCE: 05501-0211 (43150-286808)
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/618,839
C--> 12 <141> CURRENT FILING DATE: 2003-07-14
12 <150> PRIOR APPLICATION NUMBER: US 60/395,498
13 <151> PRIOR FILING DATE: 2002-07-12
15 <160> NUMBER OF SEQ ID NOS: 19
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
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26 <222> LOCATION: (207)..(1901)
27 <223> OTHER INFORMATION:
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32 <222> LOCATION: (2025)..(2025) ✓
33 <223> OTHER INFORMATION: "n" = any nucleotide
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39 <223> OTHER INFORMATION: "n" = any nucleotide
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59 atgttcatt cctgaaggac ctctccagaa tccggattgc tgaatcttcc ctgttgcccta      180
61 gaagggtccc aaaccacctc ttgaca atg gga aac tgg gtg gtt aac cac tgg      233
62                                     Met Gly Asn Trp Val Val Asn His Trp
63                                     1                               5

```

Does Not Comply
Corrected Diskette Needed

P.4

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Input Set : A:\PTO.YF.txt

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69	ttt	gtg	gat	gcc	ttc	ctg	aaa	tat	gag	aag	gcc	gac	aaa	tac	tac	tac	329
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74	Thr	Arg	Lys	Ile	Leu	Gly	Ser	Thr	Leu	Ala	Cys	Ala	Arg	Ala	Ser	Ala	
75				45					50					55			
77	ctc	tgc	ttg	aat	ttt	aac	agc	acg	ctg	atc	ctg	ctt	cct	gtg	tgt	cgc	425
78	Leu	Cys	Leu	Asn	Phe	Asn	Ser	Thr	Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	
79			60					65					70				
81	aat	ctg	ctg	tcc	ttc	ctg	agg	ggc	acc	tgc	tca	ttt	tgc	agc	cgc	aca	473
82	Asn	Leu	Leu	Ser	Phe	Leu	Arg	Gly	Thr	Cys	Ser	Phe	Cys	Ser	Arg	Thr	
83		75					80					85					
85	ctg	aga	aag	caa	ttg	gat	cac	aac	ctc	acc	ttc	cac	aag	ctg	gtg	gcc	521
86	Leu	Arg	Lys	Gln	Leu	Asp	His	Asn	Leu	Thr	Phe	His	Lys	Leu	Val	Ala	
87	90				95					100					105		
89	tat	atg	atc	tgc	cta	cat	aca	gct	att	cac	atc	att	gca	cac	ctg	ttt	569
90	Tyr	Met	Ile	Cys	Leu	His	Thr	Ala	Ile	His	Ile	Ile	Ala	His	Leu	Phe	
91					110					115					120		
93	aac	ttt	gac	tgc	tat	agc	aga	agc	cga	cag	gcc	aca	gat	ggc	tcc	ctt	617
94	Asn	Phe	Asp	Cys	Tyr	Ser	Arg	Ser	Arg	Gln	Ala	Thr	Asp	Gly	Ser	Leu	
95			125					130					135				
97	gcc	tcc	att	ctc	tcc	agc	cta	tct	cat	gat	gag	aaa	aag	ggg	ggt	tct	665
98	Ala	Ser	Ile	Leu	Ser	Ser	Leu	Ser	His	Asp	Glu	Lys	Lys	Gly	Gly	Ser	
99			140					145					150				
101	tgg	cta	aat	ccc	atc	cag	tcc	cga	aac	acg	aca	gtg	gag	tat	gtg	aca	713
102	Trp	Leu	Asn	Pro	Ile	Gln	Ser	Arg	Asn	Thr	Thr	Val	Glu	Tyr	Val	Thr	
103		155					160					165					
105	ttc	acc	agc	ggt	gct	ggt	ctc	act	gga	gtg	atc	atg	aca	ata	gcc	ttg	761
106	Phe	Thr	Ser	Val	Ala	Gly	Leu	Thr	Gly	Val	Ile	Met	Thr	Ile	Ala	Leu	
107	170				175					180					185		
109	att	ctc	atg	gta	act	tca	gct	act	gag	ttc	atc	cgg	agg	agt	tat	ttt	809
110	Ile	Leu	Met	Val	Thr	Ser	Ala	Thr	Glu	Phe	Ile	Arg	Arg	Ser	Tyr	Phe	
111					190					195					200		
113	gaa	gtc	ttc	tgg	tat	act	cac	cac	ctt	ttt	atc	ttc	tat	atc	ctt	ggc	857
114	Glu	Val	Phe	Trp	Tyr	Thr	His	His	Leu	Phe	Ile	Phe	Tyr	Ile	Leu	Gly	
115			205						210				215				
117	tta	ggg	att	cac	ggc	att	ggt	gga	att	gtc	cgg	ggt	caa	aca	gag	gag	905
118	Leu	Gly	Ile	His	Gly	Ile	Gly	Gly	Ile	Val	Arg	Gly	Gln	Thr	Glu	Glu	
119			220				225					230					
121	agc	atg	aat	gag	agt	cat	cct	cgc	aag	tgt	gca	gag	tct	ttt	gag	atg	953
122	Ser	Met	Asn	Glu	Ser	His	Pro	Arg	Lys	Cys	Ala	Glu	Ser	Phe	Glu	Met	
123		235					240					245					
125	tgg	gat	gat	cgt	gac	tcc	cac	tgt	agg	cgc	cct	aag	ttt	gaa	ggg	cat	1001
126	Trp	Asp	Asp	Arg	Asp	Ser	His	Cys	Arg	Arg	Pro	Lys	Phe	Glu	Gly	His	
127	250				255					260					265		
129	ccc	cct	gag	tct	tgg	aag	tgg	atc	ctt	gca	ccg	gtc	att	ctt	tat	atc	1049

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131					270					275					280		
133	tgt	gaa	agg	atc	ctc	cgg	ttt	tac	cgc	tcc	cag	cag	aag	gtt	gtg	att	1097
134	Cys	Glu	Arg	Ile	Leu	Arg	Phe	Tyr	Arg	Ser	Gln	Gln	Lys	Val	Val	Ile	
135				285					290					295			
137	acc	aag	gtt	gtt	atg	cac	cca	tcc	aaa	gtt	ttg	gaa	ttg	cag	atg	aac	1145
138	Thr	Lys	Val	Val	Met	His	Pro	Ser	Lys	Val	Leu	Glu	Leu	Gln	Met	Asn	
139			300					305					310				
141	aag	cgt	ggc	ttc	agc	atg	gaa	gtg	ggg	cag	tat	atc	ttt	gtt	aat	tgc	1193
142	Lys	Arg	Gly	Phe	Ser	Met	Glu	Val	Gly	Gln	Tyr	Ile	Phe	Val	Asn	Cys	
143		315					320					325					
145	ccc	tca	atc	tct	ctc	ctg	gaa	tgg	cat	cct	ttt	act	ttg	acc	tct	gct	1241
146	Pro	Ser	Ile	Ser	Leu	Leu	Glu	Trp	His	Pro	Phe	Thr	Leu	Thr	Ser	Ala	
147	330					335				340						345	
149	cca	gag	gaa	gat	ttc	ttc	tcc	att	cat	atc	cga	gca	gca	ggg	gac	tgg	1289
150	Pro	Glu	Glu	Asp	Phe	Phe	Ser	Ile	His	Ile	Arg	Ala	Ala	Gly	Asp	Trp	
151				350					355					360			
153	aca	gaa	aat	ctc	ata	agg	gct	ttc	gaa	caa	caa	tat	tca	cca	att	ccc	1337
154	Thr	Glu	Asn	Leu	Ile	Arg	Ala	Phe	Glu	Gln	Gln	Tyr	Ser	Pro	Ile	Pro	
155			365					370					375				
157	agg	att	gaa	gtg	gat	ggg	ccc	ttt	ggc	aca	gcc	agt	gag	gat	gtt	ttc	1385
158	Arg	Ile	Glu	Val	Asp	Gly	Pro	Phe	Gly	Thr	Ala	Ser	Glu	Asp	Val	Phe	
159			380				385					390					
161	cag	tat	gaa	gtg	gct	gtg	ctg	gtt	gga	gca	gga	att	ggg	gtc	acc	ccc	1433
162	Gln	Tyr	Glu	Val	Ala	Val	Leu	Val	Gly	Ala	Gly	Ile	Gly	Val	Thr	Pro	
163		395				400					405						
165	ttt	gct	tct	atc	ttg	aaa	tcc	atc	tgg	tac	aaa	ttc	cag	tgt	gca	gac	1481
166	Phe	Ala	Ser	Ile	Leu	Lys	Ser	Ile	Trp	Tyr	Lys	Phe	Gln	Cys	Ala	Asp	
167	410				415				420						425		
169	cac	aac	ctc	aaa	aca	aaa	aag	atc	tat	ttc	tac	tgg	atc	tgc	agg	gag	1529
170	His	Asn	Leu	Lys	Thr	Lys	Lys	Ile	Tyr	Phe	Tyr	Trp	Ile	Cys	Arg	Glu	
171				430					435					440			
173	aca	ggg	gcc	ttt	tcc	tgg	ttc	aac	aac	ctg	ttg	act	tcc	ctg	gaa	cag	1577
174	Thr	Gly	Ala	Phe	Ser	Trp	Phe	Asn	Asn	Leu	Leu	Thr	Ser	Leu	Glu	Gln	
175			445					450					455				
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178	Glu	Met	Glu	Glu	Leu	Gly	Lys	Val	Gly	Phe	Leu	Asn	Tyr	Arg	Leu	Phe	
179			460				465					470					
181	ctc	acc	gga	tgg	gac	agc	aat	att	gtt	ggg	cat	gca	gca	tta	aac	ttt	1673
182	Leu	Thr	Gly	Trp	Asp	Ser	Asn	Ile	Val	Gly	His	Ala	Ala	Leu	Asn	Phe	
183		475					480					485					
185	gac	aag	gcc	act	gac	atc	gtg	aca	ggg	ctg	aaa	cag	aaa	acc	tcc	ttt	1721
186	Asp	Lys	Ala	Thr	Asp	Ile	Val	Thr	Gly	Leu	Lys	Gln	Lys	Thr	Ser	Phe	
187	490					495				500					505		
189	ggg	aga	cca	atg	tgg	gac	aat	gag	ttt	tct	aca	ata	gct	acc	tcc	cac	1769
190	Gly	Arg	Pro	Met	Trp	Asp	Asn	Glu	Phe	Ser	Thr	Ile	Ala	Thr	Ser	His	
191				510					515				520				
193	ccc	aag	tct	gta	gtg	gga	gtt	ttc	tta	tgt	ggc	cct	cgg	act	ttg	gca	1817
194	Pro	Lys	Ser	Val	Val	Gly	Val	Phe	Leu	Cys	Gly	Pro	Arg	Thr	Leu	Ala	

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195 525 530 535
 197 aag agc ctg cgc aaa tgc tgt cac cga tat tcc agt ctg gat cct aga 1865
 198 Lys Ser Leu Arg Lys Cys Cys His Arg Tyr Ser Ser Leu Asp Pro Arg
 199 540 545 550
 201 aag gtt caa ttc tac ttc aac aaa gaa aat ttt tga gttataggaa 1911
 202 Lys Val Gln Phe Tyr Phe Asn Lys Glu Asn Phe
 203 555 560
 205 taaggacggt aatctgcatt ttgtctcttt gtatcttcag taattgagtt atagggaataa 1971
 W--> 207 **ggacggtaaat ctgcatttttgc tctcttttgc tcttcagtaa tttacttggt ctcttcaggt** 2031
 209 ttgancagtc actttaggat aagaatgtgc ctctcaagcc ttgactccct ggtattcttt 2091
 211 ttttgattgc attcaacttc gttacttgag cttcagcaac ttaagaactt ctgaagttct 2151
 213 taaagtcttg aantttctta agcccatgga tcttttctca gaaaaataac tgtaaactct 2211
 215 tctggacagc catgactgta gcaaggcttg atagcagaag tttggtggtt canaattata 2271
 217 caactaatcc caggtgattt tatcaattcc agtgttacca tctcctgagt tttggtttgt 2331
 219 aatcttttgc cctctccacc cccacagaag attttaagta gggtagcttt ttaaataaaa 2391
 221 atttattgaa taattaatga taaaacataa taataaacat aaataataaa caaaattacc 2451
 223 gagaacccca tccccatata acaccaacag tgtacatgtt tactgtcact tttgatatgg 2511
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 231 <211> LENGTH: 564
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 233 <213> ORGANISM: Homo sapiens
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 238 <223> OTHER INFORMATION: "n" = any nucleotide
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 258 1 5 10 15
 261 Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Asp Ala Phe Leu Lys
 262 20 25 30
 265 Tyr Glu Lys Ala Asp Lys Tyr Tyr Tyr Thr Arg Lys Ile Leu Gly Ser
 266 35 40 45
 269 Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe Asn Ser
 270 50 55 60
 273 Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser Phe Leu Arg

*These do not apply to
 this sequence. Only
 564 residues in this
 sequence; it is also
 a peptide sequence*

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274	65					70				75				80		
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278					85					90				95		
281	Asn	Leu	Thr	Phe	His	Lys	Leu	Val	Ala	Tyr	Met	Ile	Cys	Leu	His	Thr
282				100					105					110		
285	Ala	Ile	His	Ile	Ile	Ala	His	Leu	Phe	Asn	Phe	Asp	Cys	Tyr	Ser	Arg
286			115					120					125			
289	Ser	Arg	Gln	Ala	Thr	Asp	Gly	Ser	Leu	Ala	Ser	Ile	Leu	Ser	Ser	Leu
290		130					135					140				
293	Ser	His	Asp	Glu	Lys	Lys	Gly	Gly	Ser	Trp	Leu	Asn	Pro	Ile	Gln	Ser
294	145					150					155					160
297	Arg	Asn	Thr	Thr	Val	Glu	Tyr	Val	Thr	Phe	Thr	Ser	Val	Ala	Gly	Leu
298					165					170					175	
301	Thr	Gly	Val	Ile	Met	Thr	Ile	Ala	Leu	Ile	Leu	Met	Val	Thr	Ser	Ala
302				180					185					190		
305	Thr	Glu	Phe	Ile	Arg	Arg	Ser	Tyr	Phe	Glu	Val	Phe	Trp	Tyr	Thr	His
306			195					200					205			
309	His	Leu	Phe	Ile	Phe	Tyr	Ile	Leu	Gly	Leu	Gly	Ile	His	Gly	Ile	Gly
310		210					215						220			
313	Gly	Ile	Val	Arg	Gly	Gln	Thr	Glu	Glu	Ser	Met	Asn	Glu	Ser	His	Pro
314	225					230					235					240
317	Arg	Lys	Cys	Ala	Glu	Ser	Phe	Glu	Met	Trp	Asp	Asp	Arg	Asp	Ser	His
318					245					250					255	
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322				260					265					270		
325	Ile	Leu	Ala	Pro	Val	Ile	Leu	Tyr	Ile	Cys	Glu	Arg	Ile	Leu	Arg	Phe
326			275					280					285			
329	Tyr	Arg	Ser	Gln	Gln	Lys	Val	Val	Ile	Thr	Lys	Val	Val	Met	His	Pro
330		290					295					300				
333	Ser	Lys	Val	Leu	Glu	Leu	Gln	Met	Asn	Lys	Arg	Gly	Phe	Ser	Met	Glu
334	305					310					315					320
337	Val	Gly	Gln	Tyr	Ile	Phe	Val	Asn	Cys	Pro	Ser	Ile	Ser	Leu	Leu	Glu
338					325					330					335	
341	Trp	His	Pro	Phe	Thr	Leu	Thr	Ser	Ala	Pro	Glu	Glu	Asp	Phe	Phe	Ser
342				340					345					350		
345	Ile	His	Ile	Arg	Ala	Ala	Gly	Asp	Trp	Thr	Glu	Asn	Leu	Ile	Arg	Ala
346			355					360					365			
349	Phe	Glu	Gln	Gln	Tyr	Ser	Pro	Ile	Pro	Arg	Ile	Glu	Val	Asp	Gly	Pro
350		370					375					380				
353	Phe	Gly	Thr	Ala	Ser	Glu	Asp	Val	Phe	Gln	Tyr	Glu	Val	Ala	Val	Leu
354	385					390					395					400
357	Val	Gly	Ala	Gly	Ile	Gly	Val	Thr	Pro	Phe	Ala	Ser	Ile	Leu	Lys	Ser
358					405					410					415	
361	Ile	Trp	Tyr	Lys	Phe	Gln	Cys	Ala	Asp	His	Asn	Leu	Lys	Thr	Lys	Lys
362				420					425					430		
365	Ile	Tyr	Phe	Tyr	Trp	Ile	Cys	Arg	Glu	Thr	Gly	Ala	Phe	Ser	Trp	Phe
366			435					440					445			
369	Asn	Asn	Leu	Leu	Thr	Ser	Leu	Glu	Gln	Glu	Met	Glu	Glu	Leu	Gly	Lys
370		450					455					460				

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2025,2036,2164,2264

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7

VERIFICATION SUMMARY

DATE: 07/25/2003

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\07252003\J618839.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:36 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1971
M:341 Repeated in SeqNo=1
L:412 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:409
L:734 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:731
L:1056 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:1053
L:1388 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:1385
L:1714 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:1711
L:2570 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:2567